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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,126

DATE: 10/29/2001

TIME: 15:35:51

Input Set : A:\2001-10-09 3631-0108P.txt  
Output Set: N:\CRF3\10292001\I787126.raw

4 <110> APPLICANT: M&E Biotech A/S  
5 HALKIER, Torben  
6 HAANING, Jesper  
8 <120> TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand  
9 Activity  
11 <130> FILE REFERENCE: 3631-0108P  
13 <140> CURRENT APPLICATION NUMBER: US 09/787,126  
C--> 14 <141> CURRENT FILING DATE: 2001-10-09 of  
16 <160> NUMBER OF SEQ ID NOS: 36  
18 <170> SOFTWARE: PatentIn Ver. 2.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 2271  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
25 <220> FEATURE:  
26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (185)..(1138)  
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31 aaagccgggc tccaaatcg cgcccccacgt cgaggctcg cccgacgcctc cggaggttggc 120  
32 cgcacacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gaggggcag 180  
33 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229  
34 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser  
35 1 5 10 15  
36 gag gag atg ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277  
37 Glu Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His  
38 20 25 30  
39 gcc ccg ccg cct gcg ccg cac cag ccc ccc gcc tcc cgc tcc 325  
40 Ala Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser  
41 35 40 45  
42 atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373  
43 Met Phe Val Ala Leu Leu Gly Leu Gly Gln Val Val Cys Ser  
44 50 55 60  
45 gtc gcc ctg ttc tat ttc aga gcg cag atg gat cct aat aga ata 421  
46 Val Ala Leu Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
47 65 70 75  
48 tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469  
49 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu  
50 80 85 90 95  
51 aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517  
52 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu  
53 100 105 110  
54 ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg 565  
55 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val  
56 115 120 125  
57 caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag 613  
58 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu

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59	130	135	140	
60	aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag			661
61	Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys			
62	145	150	155	
63	ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc			709
64	Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile			
65	160	165	170	175
66	cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg			757
67	Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg			
68	180	185	190	
69	ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata			805
70	Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile			
71	195	200	205	
72	gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga			853
73	Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg			
74	210	215	220	
75	cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg			901
76	His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met			
77	225	230	235	
78	gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg			949
79	Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu			
80	240	245	250	255
81	atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat			997
82	Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His			
83	260	265	270	
84	ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag			1045
85	Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu			
86	275	280	285	
87	gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag			1093
88	Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln			
89	290	295	300	
90	gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga			1138
91	Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp			
92	305	310	315	
93	gccccagttt ttggagtgtt atgtatttcc tggatgtttt gaaacatttt taaaaacaag			1198
94	ccaagaaaaga tgtatataagg tgggtgagac tactaagagg catggcccca acggatcacg			1258
95	actcagtatc catgctcttg accttggata gaacacgcgt atttacagcc agtgggagat			1318
96	gttagactca tgggtgtta cacaatggtt tttaaatttt gtaatgaatt cctagaatta			1378
97	aaccagattt gggcaattttt ggttgacact tatgagaaac tgcattgtgg ctatgggagg			1438
98	gggtggccc tggcatgtt ccccttcgca gctgaagtgg agagggtgtc atctagcgc			1498
99	atggaaaggat catctgaagg ggcaattttt ttgttattttt tacatcatgc tggacactgc			1558
100	aaaaaaatact ttttctaatttggaggagaaaa atatatgtat ttttatataaa tatctaaagt			1618
101	tatattttcag atgtaatgtt ttctttgcattt agtattgtaa attatatttt tgctatagta			1678
102	tttgcatttca aatattttaaa aatgtcttgc tggatgcata tttaatgttt taaatgtaca			1738
103	gacatattta actgggtgcac ttgtttaattt ccctggggaa aacttgcagc taaggagggg			1798
104	aaaaaaatgt tggatgcata tatcaatgc agtattttt ttctttttt ttaatgtttt			1858
105	agattttttc agacttgcac agcctgtgc aaaaaattaa aatggatgcc ttgatataata			1918
106	agcaggatgt tggccaccag gtgcctttca aatttagaaa ctaattgtact ttgaaagct			1978
107	gacattqcca aaaaqgatac ataatggggcc actgaaatct gtcaagagta gttatataat			2038

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108 tggtaaacag gtgttttcc acaaagtccg caaatgtac ctttttttt ttttcaaaaat 2098  
 109 agaaaagtta ttatgtgtt atcagcaaaa aagtccaaatt ttaattttagt aaatgttac 2158  
 110 ttatactgtt caataaaaaac attgcctttg aatgttaatt ttttggtaca aaaataaaatt 2218  
 111 tataatggaaaa aaaaaaaaaa agggcggccg ctctagaggg ccctattctt tag 2271  
 114 <210> SEQ ID NO: 2  
 115 <211> LENGTH: 317  
 116 <212> TYPE: PRT  
 117 <213> ORGANISM: Homo sapiens  
 119 <400> SEQUENCE: 2  
 120 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu  
 121 1 5 10 15  
 122 Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala  
 123 20 25 30  
 124 Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met  
 125 35 40 45  
 126 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val  
 127 50 55 60  
 128 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser  
 129 65 70 75 80  
 130 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
 131 85 90 95  
 132 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
 133 100 105 110  
 134 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
 135 115 120 125  
 136 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
 137 130 135 140  
 138 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
 139 145 150 155 160  
 140 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
 141 165 170 175  
 142 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
 143 180 185 190  
 144 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
 145 195 200 205  
 146 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 147 210 215 220  
 148 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
 149 225 230 235 240  
 150 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
 151 245 250 255  
 152 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
 153 260 265 270  
 154 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
 155 275 280 285  
 156 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 157 290 295 300  
 158 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 159 305 310 315

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162 <210> SEQ ID NO: 3  
 163 <211> LENGTH: 951  
 164 <212> TYPE: DNA  
 165 <213> ORGANISM: Mus musculus  
 167 <220> FEATURE:  
 168 <221> NAME/KEY: CDS  
 169 <222> LOCATION: (1)..(951)  
 171 <220> FEATURE:  
 172 <221> NAME/KEY: misc\_feature  
 173 <222> LOCATION: (142)..(213)  
 174 <223> OTHER INFORMATION: Transmembrane domain  
 176 <220> FEATURE:  
 177 <221> NAME/KEY: misc\_feature  
 178 <222> LOCATION: (454)..(948)  
 179 <223> OTHER INFORMATION: Tumour Necrosis Factor(TNF)-like domain  
 181 <400> SEQUENCE: 3  
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 183 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu  
 184 1 5 10 15  
 185 gag atg ggc agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc 96  
 186 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro  
 187 20 25 30  
 188 gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc 144  
 189 Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser  
 190 35 40 45  
 191 atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc 192  
 192 Met Phe Leu Ala Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
 193 50 55 60  
 194 atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata 240  
 195 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
 196 65 70 75 80  
 197 tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa 288  
 198 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
 199 85 90 95  
 200 aac gca ggt ttg cag gac act ctg gag agt gaa gac aca cta cct 336  
 201 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
 202 100 105 110  
 203 gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag 384  
 204 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
 205 115 120 125  
 206 gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct 432  
 207 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala  
 208 130 135 140  
 209 atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag 480  
 210 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
 211 145 150 155 160  
 212 gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc cca tcg 528  
 213 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser  
 214 165 170 175

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215 ggt tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg 576  
 216 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp  
 217 180 185 190  
 218 gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac 624  
 219 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
 220 195 200 205  
 221 caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat 672  
 222 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
 223 210 215 220  
 224 gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg gtg tat 720  
 225 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
 226 225 230 235 240  
 227 gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa 768  
 228 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys  
 229 245 250 255  
 230 gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat 816  
 231 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 232 260 265 270  
 233 tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att 864  
 234 Ser Ile Asn Val Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
 235 275 280 285  
 236 agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg 912  
 237 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
 238 290 295 300  
 239 acg tac ttt ggg gct ttc aaa gtt cag gac ata gac tga 951  
 240 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 241 305 310 315  
 244 <210> SEQ ID NO: 4  
 245 <211> LENGTH: 316  
 246 <212> TYPE: PRT  
 247 <213> ORGANISM: Mus musculus  
 249 <400> SEQUENCE: 4  
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 253 20 25 30  
 254 Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser  
 255 35 40 45  
 256 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
 257 50 55 60  
 258 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
 259 65 70 75 80  
 260 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
 261 85 90 95  
 262 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
 263 100 105 110  
 264 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
 265 115 120 125  
 266 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date